Claims

What is claimed is:

1. A method of producing a sub-population of labeled nucleic acids, said method comprising:

(a) synthesizing first strand cDNA from a sample of RNA through reverse transcription, wherein the sample of RNA is obtained from a physiological source;

(b) contacting said first strand cDNA with a pool of a representational number of at least 15 distinct gene specific primers under conditions that allow formation of hybrid duplexes between said gene specific primers and said first strand cDNA, wherein each constituent gene specific primer has a sequence complementary to a distinct first strand cDNA; and

(c) enzymatically extending said gene specific primers from said hybrid duplexes to generate a sub-population of labeled nucleic acids.

2. The method of claim 1, wherein said sub-population of labeled nucleic acids extended from said gene specific primers is generated through a single cycle of uni-directional DNA polymerization.

3. The method of claim 1, wherein said sub-population of labeled nucleic acids extended from said gene specific primers is generated through multiple cycles of uni-directional DNA polymerization.

4. The method of claim 1, wherein said sample of RNA comprises total RNA.

5. The method of claim 1, wherein said sample of RNA comprises mRNA.

6. The method of claim 1, wherein said sample of RNA comprises amplified antisense RNA (aRNA).

7. The method of claim 1, wherein said first strand cDNA is synthesized through RNA self-priming without addition of any exogenous synthetic primers.

8. The method of claim 1, wherein said first strand cDNA is synthesized through addition of synthetic random primers.

9. The method of claim 1, wherein said first strand cDNA is synthesized through addition of oligo dT primers.

10. The method of claim 1, wherein said pool of gene specific primers comprises at least 20 distinct gene specific primers.

11. The method of claim 1, wherein said pool of gene specific primers comprises at least 50 distinct gene specific primers.

12. The method of claim 1, wherein said pool of gene specific primers comprises one oligonucleotide sequence for a single gene.

13. The method of claim 1, wherein said pool of gene specific primers comprises more than one oligonucleotide sequences for a single gene.

14. The method of claim 1, wherein the said label is directly detectable.

15. The method of claim 1, wherein the said label is detectable after a subsequent chemical or enzymatic reaction.

16. A method of producing a sub-population of labeled nucleic acids, said method comprising:

(a) synthesizing first strand cDNA from a sample of RNA through reverse transcription, wherein the sample of RNA is obtained from a physiological source;

(b) generating a sub-population of labeled nucleic acids using polymerase chain reaction (PCR) with a pool of a representational number of at least 15 pairs of distinct gene specific primers, wherein one gene specific primer in each pair comprises a sequence complementary to the sense sequence of said distinct gene, and the other primer in the pair comprises a sequence complementary to the antisense sequence of said distinct gene.

17. The method of claim 16, wherein said PCR is an asymmetric PCR.

18. The method of claim 16, wherein said PCR is performed in one cycle.

19. The method of claim 16, wherein said PCR is performed in multiple cycles.

20. The method of claim 16, wherein said sample of RNA comprises total RNA.

21. The method of claim 16, wherein said sample of RNA comprises mRNA.

22. The method of claim 16, wherein said sample of RNA comprises amplified antisense RNA (aRNA).

23. The method of claim 16, wherein said first strand cDNA is synthesized through RNA self-priming without addition of any exogenous synthetic primers.

24. The method of claim 16, wherein said first strand cDNA is synthesized through addition of synthetic random primers.

25. The method of claim 16, wherein said first strand cDNA is synthesized through addition of oligo dT primers.

26. The method of claim 16, wherein said pool of gene specific primers comprises at least 20 distinct gene specific primers.

27. The method of claim 16, wherein said pool of gene specific primers comprises at least 50 distinct gene specific primers.

28. The method of claim 16, wherein the said label is directly detectable.

29. The method of claim 16, wherein the said label is detectable after a subsequent chemical or enzymatic reaction.

30. A method of analyzing the differences in the expression pattern of the genes of special interest between a plurality of different physiological samples, said method comprising:

(a) synthesizing first strand cDNA from a sample of RNA through reverse transcription, wherein the sample of RNA is obtained from a physiological source;

(b) contacting a pool of a representational number of at least 15 distinct gene specific primers with said first strand cDNA under conditions that allow formation of hybrid duplexes between said gene specific primers and said

first strand cDNA, wherein each constituent gene specific primer has a sequence complementary to a distinct first strand cDNA; and

(c) enzymatically extending said gene specific primers from said hybrid duplexes to generate a sub-population of labeled nucleic acids and

(d) comparing the populations of labeled nucleic acids from each physiological source to identify the differences in the populations.

31. The method of claim 30, wherein the comparing step comprises:

hybridizing the labeled nucleic acids from each of the distinct physiological samples to an array of nucleic acids stably associated with the surface of a substrate;

washing off the unbound labeled nucleic acids from the surface to produce a detectable hybridization patterns for each of the distinct physiological samples; and

comparing the hybridization patterns for each of the distinct physiological samples.

32. A method of analyzing the differences in the expression pattern of the genes of special interest between a plurality of different physiological samples, said method comprising:

(a) synthesizing first strand cDNA from a sample of RNA through reverse transcription, wherein the sample of RNA is obtained from a physiological source;

(b) generating a sub-population of labeled nucleic acids using polymerase chain reaction (PCR) with a pool of a representational number of at least 15 pairs of distinct gene specific primers, wherein one gene specific primer in each pair comprises a sequence complementary to the sense sequence of said distinct gene, and the other primer in the pair comprises a sequence complementary to the antisense sequence; and

(c) comparing the populations of labeled nucleic acids from each physiological source to identify the differences in the populations.

33. The method of claim 32, wherein the comparing step comprises:

hybridizing the labeled nucleic acids from each of the distinct physiological samples to an array of nucleic acids stably associated with the surface of a substrate;

washing off the unbound labeled nucleic acids from the surface to produce a detectable hybridization patterns for each of the distinct physiological samples; and

comparing the hybridization patterns for each of the distinct physiological samples.

34. The method of claim 32, wherein said PCR is an asymmetric PCR.

35. The method of claim 32, wherein said PCR is performed in multiple cycles.